

FOR OFFICIAL USE ONLY

ACCESS DB # 153572
PLEASE PRINT CLEARLY

Scientific and Technical Information Center

CRFE

SEARCH REQUEST FORM

Requester's Full Name: TERRA GIBBS Examiner #: 79523 Date: 5/16/05
Art Unit: 1635 Phone Number: 2-0758 Serial Number: 10/005,337
Location (Bldg/Room#): 2D10 (Mailbox #): 2018 Results Format Preferred (circle): PAPER DISK

Remsen

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

ME

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Date: _____

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

I am not sure if this can be done...

Attached as Exhibit B is a nucleotide sequence ~250 bp in length

Applicants have provided this BLAST search with a result of ^{see Query¹}
comparison

completed
5-25-05

Barb O'Brien
22518

83% identity.

1. I need the same comparison with a result of 90% identity

with SEQ ID No: 2 (nucleobases 1715 - 2060) as Exhibit B shows
↓ USSN 10/005,337

2. I also need the same comparison with a result of 93% identity
with SEQ ID No: 1 NA - 2358 - this is confusing

THIS PAGE BLANK (USPTO)

Terra,

Seq 1 has 100% local similarity with "Query 1".

Seq 1 is much longer than Query 1, so the overall query match is low & can't be improved significantly.

I tried 8 different sets of parameter changes (altering Gap penalty &/or Gap size penalty) to get the best match between Seq 2, nt 1715 - 5066 vs Query 1. The best I could come up with was 82.5% Best Local Similarity (green tab).

Please let me know if you have questions.

Barb

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:32:23 ; Search time 0.001 Seconds
(without alignments)
1589.292 Million cell updates/sec

Title: US-10-005-337A-1-COPY
Perfect score: 2358
Sequence: 1 ggaatccttcatgtttaaca.....caggtcggaggccaccattgg 2358

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : new.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	337	14.3	337	1	QUERY_1 Entered [bobyren
2	17.4	0.7	337	1	QUERY_1 Entered [bobyren

ALIGNMENTS

RESULT 1					
QUERY_1 ; Entered [bobyren 25-May-05 16:13]					
QUERY_1					
Query Match 14.3%; Score 337; DB 1; Length 337;					
Best Local Similarity 100.0%; Pred. No. 0;					
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1972	GCAATATTACAGGAGCTGCTCCCTGGCTTCCGATACGTGGGATCGCATTTGCTG 2031			
DB	1	GCAATATTACAGGAGCTGCTCCCTGGCTTCCGATACGTGGGATCGCATTTGCTG 60			
QY	2032	AGCGGTGCTGCTCACTGCCAAAGGAATGACCCCTCTCACATTTCTCTGATTCGCATACGC 2091			
DB	61	AGCGGTGCTGCTCACTGCCAAAGGAATGACCCCTCTCACATTTCTCTGATTCGCATACGC 120			
QY	2092	CGGGGCGAGCTGTGATCTCCCTTTGGGCTTCCGACACTAAGTCTGGAATGAAATTT 2151			
DB	121	CGGGGCGAGCTGTGATCTCCCTTTGGGCTTCCGACACTAAGTCTGGAATGAAATTT 180			
QY	2152	CACCTCCCTCTGAATTTGGGCACCTGGTGGGGGAGGGGTGTGACTTGGCTTCCAGGCTGG 2211			
DB	181	CACCTCCCTCTGAATTTGGGCACCTGGTGGGGGAGGGGTGTGACTTGGCTTCCAGGCTGG 240			
QY	2212	AAAGATTATCTCACCAGCCCTAGCTATATAACGGGCTGGTGGAGGGGCTCCACAGGCG 2271			

Db	241	AAAGATTATCTCACCAGCCCTAGCTATATAACGGGCTGGTGGAGGGGCTCCACAGGCG 300			
QY	2272	CAGTTCACAGGGGTTTCATCCACAGAGAGAGAAAAACATA 2308			
Db	301	CAGTTCACAGGGGTTTCATCCACAGAGAGAGAAAAACATA 337			

RESULT 2
QUERY_1/c
; Entered [bobyren 25-May-05 16:13]
QUERY_1

Query Match 0.7%; Score 17.4; DB 1; Length 337;
Best Local Similarity 53.7%; Pred. No. 0;
Matches 36; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1709 CAGGGCCATTTAGCTGCAGACATCACTCCAGAGATTTCCAAACAGATAGACAAGTGG 1768
DB 186 CAGGTGAATTTTCATTCCAGACTTAGTGTCTGGGAAGCCCAAGAGGGGAGATGACAAGCTG 127
QY 1769 CACCCAG 1775
DB 126 GCCGGCG 120

Search completed: May 25, 2005, 16:32:23
Job time : 0.001 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:32:23 ; Search time 0.001 Seconds
(without alignments)
233.204 Million cell updates/sec

Title: US-10-005-337A-2_1715-2060
Perfect score: 346
Sequence: 1 gcaatgtcaacagacagctg.....cgacagaaaaacatacaaga 346

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : new.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198.2	57.3	337	1	QUERY_1 Entered [bobyren
2	12.8	3.7	337	1	QUERY_1 Entered [bobyren

ALIGNMENTS

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:34:51 ; Search time 0.872041 Seconds
(without alignments)
1.822 Million cell updates/sec

Title: US-10-005-337A-1-COPY
Perfect score: 2358
Sequence: 1 ggaatcctttcatgtttaaca.....caggtcgaggccaccattgg 2358

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : new.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	337	14.3	337	1	QUERY_1
2	21.4	0.9	337	1	QUERY_1

ALIGNMENTS

RESULT 1					
QUERY_1					
; Entered [bobyren 25-May-05 16:13]					
QUERY_1					
Query Match 14.3%; Score 337; DB 1; Length 337;					
Best Local Similarity 100.0%; Pred. No. 0;					
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1972	GCAATATTAAACAGGACGTGTCCTCGCTTCCGATACGTGGGATGACTCCGATTGCTG	2031		
DB	1	GCAATATTAAACAGGACGTGTCCTCGCTTCCGATACGTGGGATGACTCCGATTGCTG	60		
QY	2032	ACGGGTGGTCACTGCCAAAGAAATGACCCCTCAATTTCTTCTGATTCGCATAGCC	2091		
DB	61	ACGGGTGGTCACTGCCAAAGAAATGACCCCTCAATTTCTTCTGATTCGCATAGCC	120		
QY	2092	CGCGGCCAGCTTGTATCTCCCTCTGGGCTTCCGACACTAGCTCTGGAATGAAATT	2151		
DB	121	CGCGGCCAGCTTGTATCTCCCTCTGGGCTTCCGACACTAGCTCTGGAATGAAATT	180		
QY	2152	CACCTGCCCTCTGAATGGGCACCTGGTGGGGGAGGGGTGACTTGGCTTCCAGGCTGG	2211		
DB	181	CACCTGCCCTCTGAATGGGCACCTGGTGGGGGAGGGGTGACTTGGCTTCCAGGCTGG	240		
QY	2212	AAAGATTATCTACCCAGCCCTAGCTATATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGC	2271		

Db	241	AAAGATTATCTACCCAGCCCTAGCTATATATAACGGGCTGGTGTGGAGGGGCTCCACAGGC	300		
QY	2272	CAGTTCCAGGGGTTTCATCCACAAGAGAGAAAAACATA	2308		
Db	301	CAGTTCCAGGGGTTTCATCCACAAGAGAGAAAAACATA	337		
RESULT 2					
QUERY_1/c					
; Entered [bobyren 25-May-05 16:13]					
QUERY_1					
Query Match 0.9%; Score 21.4; DB 1; Length 337;					
Best Local Similarity 10.8%; Pred. No. 0;					
Matches 162; Conservative 0; Mismatches 151; Indels 1186; Gaps 5;					
QY	551	TCTTATGGTGGAGCCAGACCCATCGTGGTGGAGGAGAGCGCAACCTCACCCTCTAG	610		
DB	325	TCTTGGATGAACCCCTGGAACCTGGCCCTGTGGAGCCCTCCACACACCGCGTTATAT	266		
QY	611	CTCTGCATCCATAGCAAGTAGCTTAATGTTCTGTCTGTAGGTGTCATCTCTGTGAATCG	670		
DB	265	AGCTAGGGCTGGTGAGATATCT	242		
QY	671	AGATCCTTGGCCTTGTGAATTAGGGAGGCACAAAATACTCAGAGATTCAAGACTGCTC	730		
DB	241		242		
QY	731	AGCAGCCGAGAGTCTTCTCAAGGAAGGTCTCACTCTCAGCCCTTGTAGCTCTGA	790		
DB	241	TCCAGCCCTGGGAAGCCAAAGTCACACCCCTGCCCCACACAGTGGCC	197		
QY	791	GTGAGCCCTGGAAACAAACGCGCACAGGATGAGAAAGCTGCCATAGCTGTGTCACTT	850		
DB	196	AAITCAGAGGCGGTGAATTTTCAGACTTAGTGTCTGGGAGCC	148		
QY	851	CAAGAGGTCAAGAAAAATAGTGTAAACCATGAAAAACGAGAAGACCAAGTTATCATTTG	910		
DB	147	CAAGAGGAGATGACAA	131		
QY	911	ATAGGTCTCAGGACAGATAGACAGAGAGAACACTAGGAGAGGGGACCCAGGAGGAC	970		
DB	130		131		
QY	971	AAGGTATTAGTGTGTGTTTTCAGGGCAATCTCTGTGTACTGAAGATTCTAGAAACACAA	1030		
DB	130		131		
QY	1031	TTTGTGTTGAACAGCTGAAGTGGGTGGGGTTCTTACCCCATGTTCATGGAAGGTG	1090		
DB	130		131		
QY	1091	AGTGAAGAGACAGATATATATGATGGCCAGCATAAACAACATACACACCCCTAATTAA	1150		
DB	130		131		
QY	1151	CACCTCCCTCTTCTACTGACACCCCTTCACTCTCTCTTTTCATAAAAAATAAAAAAGT	1210		
DB	130		131		
QY	1211	ATTTTATGTGGCTTTACGATAGAAATCTTTCTCGAACTATAAAAAAGATCTAAATATTTA	1270		
DB	130		131		
QY	1271	TATTTTTCATTTTAAATATCTTAGGATGACAGCCAGAAACAAGATATTTTTCCTCT	1330		
DB	130		131		
QY	1331	CTCAACAGCAAGCTTGGGGCTTTTGTTCCTGGTGTAGGAATAGAACACGAGAGCCCC	1390		
DB	130	GCTGGCGCGCGGTATCGGAATCAGGA	101		

QY 1391 GTGTATCTAGGCAGATGCTCTATCAATTAGCCCATGAGTCTCCAGCCTCAGACGCACATTT 1450
Db 100 ----- 101
QY 1451 TTCTCGGGCTCTTAAAGCTTTTCCACAGCAATGGGAAACTTTACTGACAGCATCCAAG 1510
Db 100 ----- 101
QY 1511 TTGTGCTTCTGCTAAGAACTGGAACTGACATCTCTCTGTGATCAGTCTGGCCCGGTTTGG 1570
Db 100 ----- 101
QY 1571 GGTAGATCTCTGATTAGCCTTCAGATTTAGAACGGTGAGCCTGTGTGCACTAATTA 1630
Db 100 ----- 101
QY 1631 TGGCCAGTGACACCATAGAGTCAAGTGCATTAAGTCTTTCAATTTCTCTAATGC 1690
Db 100 ----- 101
QY 1691 TGGTACGATGGCATGTCAAGGCCCAATTTAGCTGCAGACATCACTCCAGAGAAATCCAA 1750
Db 100 ----- 64
QY 1751 ACAGATAGACAAAGTGGCAACCAGACCCATCTCTTCCCTCGGCTGATTATCCCCAG 1810
Db 63 ----- 64
QY 1811 AATAGGATGTCCAAAGCAACAATTTCCAGCCAATGGAGTGTGATAAGTCCAGTTAT 1870
Db 63 ----- 64
QY 1871 CAGAAAGATATGGCTGTAGTGTGATGCACAGTGTTCATTTCTTGATACGTTAGTCA 1930
Db 63 ----- 64
QY 1931 TATGAGAGCTGACAAAGAGGAAAGAGCAGCGATGTGTGCAATATTAAACAGGCAGCT 1990
Db 63 ----- 64
QY 1991 GTCCCTCGGCTTCCGATAGCTGGGATGACTCGCATTTGTGAGCGGTGTGTCACTGCC 2049
Db 63 ----- 13
Search completed: May 25, 2005, 16:34:53
Job time : 1.87204 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:34:51 ; Search time 0.127959 Seconds
(without alignments)
1.822 Million cell updates/sec

Title: US-10-005-337A-2_1715-2060
Perfect score: 346
Sequence: 1 gcaatgtcaacagacagctg.....cgacagaaaaacatacaaga 346

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.0

Searched: 1 segs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : new.seq:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	202.2	58.4	337	1 QUERY_1	Entered [bobryen
2	15	4.3	337	1 QUERY_1	Entered [bobryen

ALIGNMENTS

RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]

Query Match 58.4%; Score 202.2; DB 1; Length 337;
Best Local Similarity 80.8%; Pred. No. 0;
Matches 277; Conservative 0; Mismatches 58; Indels 8; Gaps 4;
QY 1 GCAATGTCAACAGACAGCTGTCCCTGAC-TCTTGACAAATAGGATGACCTTGCATTGCTG 59
Db 1 GCAATATTACAGGAGCTGTCCCTGGCTTCGGATACGTGGGATGACTCGCATTTGCTG 60
QY 60 AGCGATGTATCATCACCAAGGAATGGCCCTCTCAATTTCTTCGTATCATATTC 119
Db 61 AGCGGTGTGTCACTGCCAAAGGAATGACCTCTCAATTTCTTCTGATTGACATACGC 120
QY 120 AGCAGGGTGTAGTTGTCTCCCTCCCTCTTACAGTTCACAGACACTGAGTCTGGAATGA 179
Db 121 CGCGG-----CCAGCTGTGTCATCTCCCTCTTGGGCTTCCAGACACTAAGTCTGGAAATGA 175
QY 180 AAATTCACCTGCTCTGAGTTGGCTCTTAATGGGGCGGGAGTGTACTTTCGGTTCCCGAG 239
Db 176 AAATTCACCTGCTCTGAAATGGCCACTGGTGGGGCAGGGGTGACTTTGGCTTCCCGAG 235
QY 240 GTTGAAGATTAATCTCACCGGCCCGCAGCTATATAAGCTGACCGGTGTGAGGGGGCCAG 299
Db 236 GCTGAAGATTAATCTCACCGGCCCTAGCTATATAA-CGGGCTGGTGTGAGGGGCTCCA 294
QY 300 CAGGGCCAACTCCAGGGATTCTTC-CACGACAGAAACATA 341
Db 295 CAGGGCCAGTTCCAGGGGTTTCATCCCAAGAGAGAAAAACATA 337

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]

Query Match 4.3%; Score 15; DB 1; Length 337;
Best Local Similarity 26.7%; Pred. No. 0;
Matches 62; Conservative 0; Mismatches 45; Indels 125; Gaps 2;
QY 85 TGGCCCTCTCACATTTCTTCTGATTCACATATTACAGCAGGGTGTAGTCTTCTCCCTC 144
Db 294 TGGAGCCCTTCCACACAGCCCGCTTATAGCTAGGGCTGGGTGAGATAATCTTCC----- 239
QY 145 CCTCTTCAGTTTCCAGACACTGAGTCTGGAATGAATAATTCACCTGCTCTGAGTTGGCT 204
Db 238 -----AGCCTGGGAAGCCAAAGTCACACCCCT----- 213
QY 205 CCTAATGGGGCGGGAGTGTACTTCCGTTCCAGGTTGGAAGATTATCTACCCCGCCC 264

Db 212 ----- 213
Qy 265 CAGCTATATAAGCTGACCGGTGTGAGGGGCCGAGGGCCCAACTCCAGGG 316
Db 212 -----GCCGCCACCACTGGCCCAATTCAGAG 188

Search completed: May 25, 2005, 16:34:53
Job time : 0.127959 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:35:35 ; Search time 0.001 Seconds
(without alignments)
1589.292 Million cell updates/sec

Title: US-10-005-337A-1-COPY
Perfect score: 2358
Sequence: 1 g9atcccttcattgttaaca.....caggtcgaggccaccattgg 2358

Scoring table: IDENTITY_NUC
Gapop 1.0 , Gapext 1.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : new.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	337	14.3	337	1	QUERY_1 Entered [bobryen]
2	40.8	1.7	337	1	QUERY_1 Entered [bobryen]

ALIGNMENTS

RESULT 1					
QUERY_1					
; Entered [bobryen 25-May-05 16:13]					
QUERY_1					
Query Match 14.3%; Score 337; DB 1; Length 337;					
Best Local Similarity 100.0%; Pred. No. 0;					
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1972	GCAATATTAAACAGGACGTGTCCCTGGCTTCCGATAGTGGGATGACTCGCAATTGCTG 2031			
DB	1	GCAATATTAAACAGGACGTGTCCCTGGCTTCCGATAGTGGGATGACTCGCAATTGCTG 60			
QY	2032	ACGGGTGTGGTCACTGCCAAAGGAATGACCTCTCACATTTCTTCTGATTCCGATACGC 2091			
DB	61	ACGGGTGTGGTCACTGCCAAAGGAATGACCTCTCACATTTCTTCTGATTCCGATACGC 120			
QY	2092	CGGGCCAGCTGTGATCTCCCTTGGGCTTCCGACACTAAGTCTGGAATGAAATT 2151			
DB	121	CGGGCCAGCTGTGATCTCCCTTGGGCTTCCGACACTAAGTCTGGAATGAAATT 180			
QY	2152	CACCTGCTCTCAATTTGGCCACTGTGGGGGAGGGGTGTGACTTGGCTTCCAGGCTGG 2211			
DB	181	CACCTGCTCTCAATTTGGCCACTGTGGGGGAGGGGTGTGACTTGGCTTCCAGGCTGG 240			
QY	2212	AAGATTATCTACCCAGCCCTAGCTATATATAACGGGCTGGTGTGGAGGGGCTCCACAGGCG 2271			

Db	241	AAAGATTATCTACCCAGCCCTAGCTATATATAACGGGCTGGTGTGGAGGGGCTCCACAGGCG 300			
QY	2272	CAGTTCCAGGGGTTTCATCCACAAGAGAGAAAAACATA 2308			
Db	301	CAGTTCCAGGGGTTTCATCCACAAGAGAGAAAAACATA 337			

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match 1.7%; Score 40.8; DB 1; Length 337;
Best Local Similarity 53.8%; Pred. No. 0;
Matches 170; Conservative 0; Mismatches 107; Indels 39; Gaps 26;
QY 2054 GAATGACCTCTCACATTTCTTCTGATTGCGATAGCGCGGCGGCGGCTTCATCTCC 2113
DB 319 GGATGAACCCCT-GGAACCTGGCCCTGTGGAGC-CCTCCAC-ACCAGCCGTTATAT--A 265
QY 2114 TCTTGGGCT-TCCAGACA--CT--AAGTCTGGAATGAAATTC-----CCTG-CCTCTG 2163
DB 264 GCTAGGGCTGGTGAGATAATCTTCCAGCTGGGAAGCCAACTCACACCCCTGCCCCAC 205
QY 2164 AATTGGCCACTGGTGGGCGAGGGGTGTGACTTCCAGCTTCCAGGCTGGAAGATTATCTCA 2223
DB 204 CAGTGGCCAAT-TCAGAGGCGAG---GTGAATTTTCATTCAGACT--TAG--TGCT-G 155
QY 2224 CCCAGCCC--TAGCTATATACGGGCTGTG-GTGAGG-GGCTCCACAGGGCCA-GTTCC 2278
DB 154 GGAAGCCCAAGAGGAGATGACAAGCTGGCCCGCGTATGCGAATCAGGAAGAAATGTG 95
QY 2279 AGGGGTTCATCCACAAGAGAG-AAAAACATAGACTCGAGGTCTAGGGAGCTTGCATGCT 2337
DB 94 AGAGGGTCAATTCCTTTGGCAGTGACCAACCG-CTC-AGCAAT-GCGAG--T-CAT-CCC 42

Search completed: May 25, 2005, 16:35:35
Job time : 0.001 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:35:35 ; Search time 0.001 Seconds
(without alignments)
233.204 Million cell updates/sec

Title: US-10-005-337A-2_1715-2060

Perfect score: 346

Sequence: 1 gcaatgtcaacagacagctg.....cgacagaaaaacatacaaga 346

Scoring table: IDENTITY_NUC

Gapop 1.0 , Gapext 1.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : new.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	238.8	69.0	337	1 QUERY_1	Entered [bobryen
2	36.8	10.6	337	1 QUERY_1	Entered [bobryen

ALIGNMENTS

RESULT 1

QUERY_1

; Entered [bobryen 25-May-05 16:13]

QUERY_1

Query Match	69.0%;	Score 238.8;	DB 1;	Length 337;
Best Local Similarity	82.5%;	Pred. No. 0;		
Matches	283;	Conservative	0;	Mismatches 52; Indels 8; Gaps 5;
QY	1	GCAATGTCAACAGACAGCTGTCCCTGAC-TCTTGACAAATAGGATGACTTGCATTGCTG	59	
Db	1	GCAATATTAAACAGCAGCTGTCCCTGGCTTCCCGATACGTGGGATGACTCGCATTTGCTG	60	
QY	60	AGCGATGTGATCACCAACGAAGGCGCTCTCACATTTCTTCTGATTCACATATTC	119	
Db	61	AGCGGTGTGGTCACTGCGAAAGGAATGACCCCTCTCACATTTCTTCTGATTCGCATACGC	120	
QY	120	AGCAGGGTTAGCTGTGCTCCCTCCCTCTTCAGCTTCCAGACACTGAGTCTGGAATGA	179	
Db	121	CGC--GGCAGCTTGTCAT---CTCCCTCTTGGGCTTCCAGACACTAAGTCTGGAATGA	175	
QY	180	AAATTACCTGCTCTGAGTTGGCTCTTAATGGGGGGGAGTGTTACTTGGTTCCCGAG	239	
Db	176	AAATTACCTGCTCTGAAATGGCCACTGGTGGGGGAGGGGTGACTTTGGCTTCCCGAG	235	
QY	240	GTGGAAGATTATCTCACCGCGCCAGCTATATAAGCTACCGGTGGAGGGGCGCCAG	299	
Db	236	GCTGGAAGATTATCTCACCGCGCCCTAGCTATATAA-CGGGCTGGTGGAGGGGCTCCA	294	
QY	300	CAGGGCCAACTCCAGGGAATTCCTTC-CACGACAGAAAAACATA	341	
Db	295	CAGGGCCAGTTCAGGGGTTTCATCCACAGAGAGAAAAACATA	337	

RESULT 2

QUERY_1/c

; Entered [bobryen 25-May-05 16:13]

QUERY_1

Query Match	10.6%;	Score 36.8;	DB 1;	Length 337;
Best Local Similarity	55.3%;	Pred. No. 0;		
Matches	146;	Conservative	0;	Mismatches 82; Indels 36; Gaps 24;
QY	42	GGATGA---CTTGCTGCTGAGGATGT-GATCACCAACCAAGGAATGGCCCTCTCACA	97	
Db	319	GGATGAACCCCTGGAA--CTG-GCCCTGTGGAGCCCTCCACACCA---GCCCGTTATA	267	
QY	98	TTTCT--TCCTGATTCACATA---TT-CAGCAGGGTTAG-CTTGTC-CTCCCT-CCCTC	148	
Db	266	TAGTAGGGCTGGGTGAGATAATCTTCCAGCCTGGGAGCCAGTCACACCCCTGCCCC	207	
QY	149	TTGAGTTCCAGACACTGAGTCTGGAAATGAAATCA--CCTGCTCTGAGT-TGG--C	203	
Db	206	ACCAG-TGGCCA-ATTGAGAGGAGG--TGAATTTTCATTCAGACTTAGTGTCTGGAA	151	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:36:21 ; Search time 0.872041 Seconds
(without alignments)
1.822 Million cell updates/sec

Title: US-10-005-337A-1-COPY
Perfect score: 2358
Sequence: 1 ggatcccttcatgtttaaca.....cagtcggaggaccaccattgg 2358

Scoring table: IDENTITY_NUC
Gapop 0.5 , Gapext 0.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : new.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	337	14.3	337	1	QUERY_1 Entered [bobryen]
2	282.5	12.0	337	1	QUERY_1 Entered [bobryen]

ALIGNMENTS

RESULT 1					
QUERY_1					
; Entered [bobryen 25-May-05 16:13]					
QUERY_1					
Query Match 14.3%; Score 337; DB 1; Length 337;					
Best Local Similarity 100.0%; Pred. No. 0;					
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1972	GCAATATTAAACAGGAGCTGTCCCTGGCTTCCGATAGCTGGGATGACTCGCATTTGCTG 2031			
Db	1	GCAATATTAAACAGGAGCTGTCCCTGGCTTCCGATAGCTGGGATGACTCGCATTTGCTG 60			
Qy	2032	ACGGTGTGGTCACTGCCAAAGAAATGACCTCTCACATTTCTTCTGATTCGCATACGC 2091			
Db	61	ACGGTGTGGTCACTGCCAAAGAAATGACCTCTCACATTTCTTCTGATTCGCATACGC 120			
Qy	2092	CGCGGCCAGCTTGTCACTCCCTCTTGGCTTCCAGACACTAAGTCTGGAATGAAATT 2151			
Db	121	CGCGGCCAGCTTGTCACTCCCTCTTGGCTTCCAGACACTAAGTCTGGAATGAAATT 180			
Qy	2152	CACCTGCTCTGAAATTTGGCCACTGTGGGGCAGGGGTGTGACTTGGCTTCCAGGCTGG 2211			
Db	181	CACCTGCTCTGAAATTTGGCCACTGTGGGGCAGGGGTGTGACTTGGCTTCCAGGCTGG 240			
Qy	2212	AAGATTATCTCAACCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGCG 2271			

Db	241																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		</
----	-----	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	----

ALIGNMENTS

RESULT 1

QUERY_1/c

; Entered [bobryen 25-May-05 16:13]

QUERY_1

Query Match 75.9%; Score 262.5; DB 1; Length 337;
Best Local Similarity 79.9%; Pred. No. 0;
Matches 290; Conservative 0; Mismatches 25; Indels 48; Gaps 25;

QY 1 GCAATGTCACAGACAGCTGTCCCT-GACTCTT---GACAAATA-----GGATGACTTGC 52
DB 1 GCAATATTAAACAGGACGCTGTCCCTGG---CTTCCG---ATACGTGGGATGACTGCG 53

QY 53 ATTGCTGAGGATGTGATCAC--CACAAAGGAATGGCCCTCTCACATTTCTTCCTGATT 110
DB 54 ATTGCTGAGCGGTGTGGTCACTGC--CAAAGGAATGACCCCTCTCACATTTCTTCCTGATT 111

QY 111 CACATATTACAGAG--GGTGTGCTGTCTCCCTCCCTCTTCAG--CTTCCCAGACACTG 167
DB 112 CGGATA--C-GCGCGCGCAGCTTGTAT---CTCCCTCTT---GGCTTCCCGACACTA 163

QY 168 AGTCTGGAATGAAATTCACCTGCTCTGAGTTGGCTC-CTAATGGGGG-CGGAGTGT 225
DB 164 AGTCTGGAATGAAATTCACCTGCTCTGAAATGGC-CACTGTGGGGGCGAGG-GTGTG 221

QY 226 ACTTCGG-TTCCAGATTGGAAGATTATCTCAGCCGCGCCAGCTATATAA---GCTGAC 281
DB 222 ACTT-GGCTTCCAGGCTGGAAGATTATCTCAGCCAGCCCTAGCTATATAACGGGCT--- 277

QY 282 CGGTGTGGAGGGG-CAGCAGGCGCAACTCCAGGGAATTCCTTCCAC--GACAGAAAAAC 338
DB 278 -GGTGTGGAGGGGCTCCA-CAGGGCCAGTTCAGGGGTT-CATCCAAAGAGAGAAAAAC 334

QY 339 ATA 341
DB 335 ATA 337

RESULT 2

QUERY_1/c

; Entered [bobryen 25-May-05 16:13]

QUERY_1

Query Match 46.1%; Score 159.6; DB 1; Length 337;
Best Local Similarity 45.2%; Pred. No. 0;
Matches 208; Conservative 0; Mismatches 9; Indels 243; Gaps 86;

QY 4 ATG--TCAACAGACAGCTGTCCCTGACTCTTGACAAATAGGATGA--CTTGCAATTGCTG 59
DB 336 ATGTTT-----T-T---CT--CTCTTG-----T-GGATGAACC--C-----CTG 307

QY 60 AGCGA--TG-----TGATCACCACCAAGGAATGGCCCTCT-CACATTTCTTCTCTGA---- 108
DB 306 ---GAAGTGGCCCTG-T-----GGA-----GCC-CTCCACA-----CC--AGCCC 273

QY 109 -TTACATATTGAGC-AGGGTTAGCT---TGTCCTCCCTCCCTCTTTCAG-----CTTCC 158
DB 272 GTT---ATAT--AGCTAGG---GCTGGGTG-----AGATAATCTT-C 240

QY 159 CAGACACTGAGTCTGGAATG--AA---AATTCA--CCTGC-----CTCTGAGTTGGCTCC 206
DB 239 CAG-C-CTG-----GGAA-GCAAGTCA---CACCCCTGCCCCAC-C--AG-TGG--CC 197

QY 207 TAAT---G-GGGGC-GG-GAGTGT-----ACTCG-GT-T-----CCC-AG-GT 241
DB 196 -AATTCAGAG--GCAGTGAAT-TTTCATTCAGACTTAGTGTCTGGGAAGCCCAAGAG- 142

QY 242 TGAAGATTATCTCA-----CC-CGGCCCCAGCTATATAAGCTGA--CCGG-----TG 286
DB 242 TGAAGATTATCTCA-----CC-CGGCCCCAGCTATATAAGCTGA--CCGG-----TG 286

DB 141 -GG-AGATGA---CAAGCTGGCCGCGGC-----G---TAT--GC-GAATCAGGAAGAAATG 97
QY 287 TG-GAGGGGC---CC---AGCAG-GGCCA-ACTC---CAG---G-GA-T--TCCTTCCA 326
DB 96 TGAGAGGGTCATTCCTTTGGCAGTGACACAC-CGCTCAGCAATGCGAGTCATC---CCA 41
QY 327 CG-A-CAGAAA--A-----ACA-----TACA-A--G 345
DB 40 CGTATCGGAAGCCAGGGGACAGCTGCTGTGTTA-ATATTG 2

Search completed: May 25, 2005, 16:36:23
Job time : 0.127959 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:37:10 ; Search time 0.872041 Seconds
(without alignments)
1.822 Million cell updates/sec

Title: US-10-005-337A-1-COPY
Perfect score: 2358
Sequence: 1 ggatccttcatgtttaa.....cagtcgaggccaccatgg 2358

Scoring table: IDENTITY_NUC
Gapop 20_0 , Gapext 0.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : new.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	337	14.3	337	1	QUERY_1 Entered [bobryen]
2	17.4	0.7	337	1	QUERY_1 Entered [bobryen]

ALIGNMENTS

RESULT 1					
QUERY_1 ; Entered [bobryen 25-May-05 16:13]					
QUERY_1					
Query Match 14.3%; Score 337; DB 1; Length 337;					
Best Local Similarity 100.0%; Pred. No. 0;					
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1972	GCATATTAAACAGGAGCTGCTCCCTGGCTCCGATAGCTGGGATGACTCGCATTTGCTG	2031		
DB	1	GCATATTAAACAGGAGCTGCTCCCTGGCTCCGATAGCTGGGATGACTCGCATTTGCTG	60		
QY	2032	ACGGGTGGTCACTGCCAAAGAAATGACCCCTCACAATTTCTTCTGATTCGCATACGC	2091		
DB	61	ACGGGTGGTCACTGCCAAAGAAATGACCCCTCACAATTTCTTCTGATTCGCATACGC	120		
QY	2092	CGGGCCAGCTTGTATCTCCCTCTGGCTTCCGACACTAAGTCTGGATGAATTT	2151		
DB	121	CGGGCCAGCTTGTATCTCCCTCTGGCTTCCGACACTAAGTCTGGATGAATTT	180		
QY	2152	CACCTGCCCTCTGAATTTGGCACTGGTGGGGCAGGGGTGTGACTTTGGCTTCCAGGCTGG	2211		
DB	181	CACCTGCCCTCTGAATTTGGCACTGGTGGGGCAGGGGTGTGACTTTGGCTTCCAGGCTGG	240		
QY	2212	AAAGATTATCTCAACCCAGCCCTAGCTATATATAACGGGCTGGTGTGGAGGGGCTCCACAGGCG	2271		

Db	241	AAAGATTATCTCAACCCAGCCCTAGCTATATATAACGGGCTGGTGTGGAGGGGCTCCACAGGCG	300		
QY	2272	CAGTTCCAGGGGTTTCATCCACAAGAGAGAAAAACATA	2308		
DB	301	CAGTTCCAGGGGTTTCATCCACAAGAGAGAAAAACATA	337		

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match 0.7%; Score 17.4; DB 1; Length 337;
Best Local Similarity 53.7%; Pred. No. 0;
Matches 36; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY	1709	CAGGGCCATTTAGCTGCAGACATCACTCCAGAGATTCCTCAACAGATAGACAAGTGG	1768		
DB	186	CAGGTGAATTTTTCATTCCAGACTTAGTGTCTGGGAAGCCCAAGAGGGAGATGACAAGCTG	127		
QY	1769	CACCCAG 1775			
DB	126	GCCGCG 120			

Search completed: May 25, 2005, 16:37:11
Job time : 0.872041 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:37:10 ; Search time 0.127959 Seconds
(without alignments)
1.822 Million cell updates/sec

Title: US-10-005-337A-2_1715-2060
Perfect score: 346
Sequence: 1 gcaatgtcaacagacagctg.....cgacagaaaaacatacaaga 346

Scoring table: IDENTITY_NUC
Gapop 20_0 , Gapext 0.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : new.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	169.6	49.0	337	1	QUERY_1 Entered [bobryen]
2	12.8	3.7	337	1	QUERY_1 Entered [bobryen]

ALIGNMENTS

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:37:50 ; Search time 0.001 Seconds
(without alignments)
1589.292 Million cell updates/sec

Title: US-10-005-337A-1-COPY
Perfect score: 2358
Sequence: 1 ggaatcctttcatgtttaaca.....cagtcgagggcaccaccatgg 2358

Scoring table: IDENTITY_NUC
Gapop 60.0 , Gapext 0.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : new.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	337	14.3	337	1 QUERY_1	Entered [bobryen]
2	17.4	0.7	337	1 QUERY_1	Entered [bobryen]

ALIGNMENTS

RESULT 1					
QUERY_1					
; Entered [bobryen 25-May-05 16:13]					
QUERY_1					
Query Match 14.3%; Score 337; DB 1; Length 337;					
Best Local Similarity 100.0%; Pred. No. 0;					
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1972	GCAATATTAAACAGGACGTCTCCCTGGCTTCCGATAGCTGGGATCGCATTTGCTG	2031		
DB	1	GCAATATTAAACAGGACGTCTCCCTGGCTTCCGATAGCTGGGATCGCATTTGCTG	60		
QY	2032	AGCGGTGGTCTACGCCAAAGAAATGACCTCTCACTTTCTCTGATTCGCATACGC	2091		
DB	61	AGCGGTGGTCTACGCCAAAGAAATGACCTCTCACTTTCTCTGATTCGCATACGC	120		
QY	2092	CGCGGCACGCTTCTATCTCCCTTGGCTTCCAGACACTAAGTCTGGAATGAAATTT	2151		
DB	121	CGCGGCACGCTTCTATCTCCCTTGGCTTCCAGACACTAAGTCTGGAATGAAATTT	180		
QY	2152	CACCTCCCTCTGAATTTGGCCACTGTGGGGGAGGGGTGTGACTTGGCTTCCAGGCTGG	2211		
DB	181	CACCTCCCTCTGAATTTGGCCACTGTGGGGGAGGGGTGTGACTTGGCTTCCAGGCTGG	240		
QY	2212	AAGATTATCTACCCAGCCCTAGCTATATAACGGGGCTGTGTGGAGGGGCTCCACAGGCG	2271		

Db	241	AAAGATTATCTACCCAGCCCTAGCTATATAACGGGGCTGTGTGGAGGGGCTCCACAGGCG	300		
QY	2272	CAGTTCCAGGGGTTTCATCCACAAGAGAGAAAAACATA	2308		
DB	301	CAGTTCCAGGGGTTTCATCCACAAGAGAGAAAAACATA	337		

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match 0.7%; Score 17.4; DB 1; Length 337;
Best Local Similarity 53.7%; Pred. No. 0;
Matches 36; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY	1709	CAGGGCCATTTTAGCTGCAGACATCACTCCAGAGATTCCAAACACATAGACAAAGTGG	1768		
DB	186	CAGGTGAATTTTCATTTCCAGACTTAGTGTCTGGGAAGCCCAAGAGGGAGATGACAAGCTG	127		
QY	1769	CACCCAG 1775			
DB	126	GCGGCGG 120			

Search completed: May 25, 2005, 16:37:51
Job time : 1 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:37:50 ; Search time 0.001 Seconds
(without alignments)
233.204 Million cell updates/sec

Title: US-10-005-337A-2 1715-2060
Perfect score: 346
Sequence: 1 gcaatgtcaacagacagctg.....cgacagaaaaacatacaaga 346

Scoring table: IDENTITY_NUC
Gapop 60.0 , Gapext 0.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : new.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	128.6	37.2	337	1 QUERY_1	Entered [bobryen]
2	12.8	3.7	337	1 QUERY_1	Entered [bobryen]

ALIGNMENTS

```
RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match      37.2%; Score 128.6; DB 1; Length 337;
Best Local Similarity 73.8%; Pred. No. 0;
Matches 236; Conservative 0; Mismatches 79; Indels 5; Gaps 1;

QY 22 CCCTGACTCTTGACAAATAGGATGACTTGCAATTGCTGAGCGATGATCACCACCAAAG 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 CCCTGCTTCCCGATACGTGGGATGACTGCAATTGCTGAGCGGTGGTCACTGCCAAAG 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 82 GAATGCCCTCTCACATTTCTTCTGATTCACATATTCAGCAGGGTTAGCTTGCTCTCC 141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 GAATGACCTCTCACATTTCTTCTGATTCGCATACGCCGGGC-----CAGCTTGTCT 137
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 142 CTCCTCTTCAGCTTCCAGACACTGAGTCTGGAATGMAAATTCACCTGCCCTGAGTTG 201
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 CTCCTCTTTGGGCTTCCAGACACTAAGTCTGGAATGMAAATTCACCTGCCCTGAAATTG 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 202 GCTCTTAATGGGGCGGGAGTGTTACTTCGGTTCCAGGTTGGAAGATTATCTCACCCGG 261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 198 GCCACTGGTGGGGCGAGGGGTGACTTGGCTTCCAGGCTGGAAGATTATCTCACCCAG 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 262 CCCAGCTATATAAGCTGACCGGTGTGGAGGGGCCCAGCAGGGCCAACTCCAGGGGATTC 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 CCCTAGCTATATAACGGGCTGTGTGGAGGGGCTCCACAGGGCCAGTTCAGGGGTTTCAT 317
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 322 TTCACGACAGAAACATA 341
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 318 CCACAAGAGAGAAAAACATA 337
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match      3.7%; Score 12.8; DB 1; Length 337;
Best Local Similarity 51.8%; Pred. No. 0;
Matches 29; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 85 TGGCCCTCTCACATTTCTTCTGATTCACATATTCAGCAGGGTTAGTTGCTCTCC 140
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 294 TGGAGCCCTCCACACAGCCCGTTATATAGCTAGGGCTGGGTGAGATAATCTTCC 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: May 25, 2005, 16:37:51
Job time : 0.001 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:38:25 ; Search time 0.872041 Seconds
(without alignments)
1.822 Million cell updates/sec

Title: US-10-005-337A-1-COPY
Perfect score: 2358
Sequence: 1 ggatcctttcatgtttaaca.....cagtcggaggccaccatgg 2358

Scoring table: IDENTITY_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : new.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	337	14.3	337	1	QUERY_1 Entered [bobryen]
2	17.4	0.7	337	1	QUERY_1 Entered [bobryen]

ALIGNMENTS

RESULT 1					
QUERY_1					
; Entered [bobryen 25-May-05 16:13]					
QUERY_1					
Query Match 14.3%; Score 337; DB 1; Length 337;					
Best Local Similarity 100.0%; Pred. No. 0;					
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1972	GCAATATTACAGGAGCTGCCCTGGCTTCCGATACGTGGGATGACTCGCATTCGTG	2031		
DB	1	GCAATATTACAGGAGCTGCCCTGGCTTCCGATACGTGGGATGACTCGCATTCGTG	60		
QY	2032	AGCGGTGTGTCACCTGCCAAAGGAATGACCCCTCTCACATTTCTCTGATTCGCATACGC	2091		
DB	61	AGCGGTGTGTCACCTGCCAAAGGAATGACCCCTCTCACATTTCTCTGATTCGCATACGC	120		
QY	2092	CGGGCCAGCTTGTATCTCCCTTGGGCTTCCGACACTAAGTCTGGAATGAAATTT	2151		
DB	121	CGGGCCAGCTTGTATCTCCCTTGGGCTTCCGACACTAAGTCTGGAATGAAATTT	180		
QY	2152	CACCTCCCTCTGAATTTGGCCACTGTGGGGAGGGGTGTGACTTGGCTTCCAGGCTGG	2211		
DB	181	CACCTCCCTCTGAATTTGGCCACTGTGGGGAGGGGTGTGACTTGGCTTCCAGGCTGG	240		
QY	2212	AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGC	2271		

Db	241	AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGC	300		
QY	2272	CAGTTCCAGGGGTTTCATCCACAAGAGAGAGAAAAACATA	2308		
DB	301	CAGTTCCAGGGGTTTCATCCACAAGAGAGAGAAAAACATA	337		

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match 0.7%; Score 17.4; DB 1; Length 337;
Best Local Similarity 53.7%; Pred. No. 0;
Matches 36; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1709 CAGGGCCATTTAGCTGCAGACATCACTCCAGAGATTTCCAAACAGATAGACAGTGG 1768
DB 186 CAGGTGAATTTTCATTTCCAGACTTAGTGTCTGGGAAGCCCAAGAGGGAGATGACAAAGCTG 127
QY 1769 CACCCAG 1775
DB 126 GCGGCGG 120

Search completed: May 25, 2005, 16:38:25
Job time : 0.872041 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:38:25 ; Search time 0.127959 Seconds
(without alignments)
1.822 Million cell updates/sec

Title: US-10-005-337A-2 1715-2060
Perfect score: 346
Sequence: 1 gcaatgtcaacagacagctg.....cgacagaaaaacatacaaga 346

Scoring table: IDENTITY_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : new.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120.8	34.9	337	1	QUERY_1 Entered [bobryen]
2	12.8	3.7	337	1	QUERY_1 Entered [bobryen]

ALIGNMENTS

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:39:04 ; Search time 0.001 Seconds
(without alignments)
1589.292 Million cell updates/sec

Title: US-10-005-337A-1-COPY
Perfect score: 2358
Sequence: 1 ggatectttcatgtttaaca.....cagtcggaggccaccatgg 2358

Scoring table: IDENTITY_NUC
Gapop 0.5 , Gapext 60.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : new.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	337	14.3	337	1	QUERY_1 Entered [bobryen
2	17.4	0.7	337	1	QUERY_1 Entered [bobryen

ALIGNMENTS

RESULT 1					
QUERY_1					
; Entered [bobryen 25-May-05 16:13]					
QUERY_1					
Query Match 14.3%; Score 337; DB 1; Length 337;					
Best Local Similarity 100.0%; Pred. No. 0;					
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1972	GCAATATTAAACAGGACAGCTGTCCCTCGGCTTCCGATACGTGGGATCGCATTTGCTG	2031		
DB	1	GCAATATTAAACAGGACAGCTGTCCCTCGGCTTCCGATACGTGGGATCGCATTTGCTG	60		
QY	2032	AGCGGTGTGGTCACTGCCAAAGGAATGACCTCTCAATTTCTTCTGATTCGCATACGC	2091		
DB	61	AGCGGTGTGGTCACTGCCAAAGGAATGACCTCTCAATTTCTTCTGATTCGCATACGC	120		
QY	2092	CGGGCCAGCTTGTCACTCCCTTTGGGCTTCCGACACTAAGTCTGGAATGAATTT	2151		
DB	121	CGGGCCAGCTTGTCACTCCCTTTGGGCTTCCGACACTAAGTCTGGAATGAATTT	180		
QY	2152	CACCTGCCCTCTGAATTTGGCCACTGTGGGGCAGGGGTGTGACTTGGCTTCCAGGCTGG	2211		
DB	181	CACCTGCCCTCTGAATTTGGCCACTGTGGGGCAGGGGTGTGACTTGGCTTCCAGGCTGG	240		
QY	2212	AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGTGTGGAGGGGCTCCACAGGCG	2271		

Db	241	AAATTATCTCACCCAGCCCTAGCTATATAACGGGCTGTGTGGAGGGCTCCACAGGCG	300		
QY	2272	CAGTTCCAGGGGTTTCATCCACAAGAGAGAAAAACATA	2308		
DB	301	CAGTTCCAGGGGTTTCATCCACAAGAGAGAAAAACATA	337		

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match 0.7%; Score 17.4; DB 1; Length 337;
Best Local Similarity 53.7%; Pred. No. 0;
Matches 36; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY	1709	CAGGGCCATTTTAGTTCGACACATCACTCCAGAGATTCCAAACAGATAGACAAAGTGG	1768		
DB	186	CAGGTGAATTTTCATTCAGACTTAGTGTCTGGGAAGCCCAAGAGGAGATGCAAGCTG	127		
QY	1769	CACCCAG 1775			
DB	126	GCGGCGG 120			

Search completed: May 25, 2005, 16:39:05
Job time : 1'secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:39:04 ; Search time 0.001 Seconds
(without alignments)
233.204 Million cell updates/sec

Title: US-10-005-337A-2_1715-2060
Perfect score: 346
Sequence: 1 gcaatgtcaacagacagctg.....cgacagaaaaacatacaaga 346

Scoring table: IDENTITY_NUC
Gapop 0.5 , Gapext 60.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : new.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120.8	34.9	337	1	QUERY_1 Entered [bobryen
2	12.8	3.7	337	1	QUERY_1 Entered [bobryen

ALIGNMENTS

